

1
SEQUENCE LISTING

<110> Hageman, Gregory S.
Kuehn, Markus H.

<120> THERAPEUTICS AND DIAGNOSTICS FOR OCULAR DISEASE BASED
ON A NOVEL HUMAN GENE FAMILY

<130> UIA-027.01

<140> 09/183,972
<141> 1998-10-29

<160> 49

<170> PatentIn Ver. 2.0

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<213> Callimico sp.

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Gln Ile Leu Ala Ser Leu Gln Ala Tyr Tyr Arg Leu Arg Val Cys Gln
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gaa gca gta tgg gaa gca tat cgg atc ttt ctg gat cgc atc cct gac 144
Glu Ala Val Trp Glu Ala Tyr Arg Ile Phe Leu Asp Arg Ile Pro Asp
35 40 45

aca ggg gaa tat cag gac tgg gtc agc ttc tgc cag cag gag acc ttc 192
Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe
50 55 60

tgc ctc ttt gac atc gga caa aac ttc agc aat tcc cag gag cac ctg 240
Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu
65 70 75 80

gat ctt ctc cag cag aga ata aaa cag aga agt ttc cct gag aga aaa 288
Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys
85 90 95

gat gaa gta tct aca gag aag aca ttg gga gag cct agt gaa acc att 336
Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile
100 105 110

gtg gtt tca aca gat gtt gcc agc gtc tca ttt ggg cct ttc cct gtc 384
Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val
115 120 125

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Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile	Leu Asp Asn Ala Leu Asn		
130	135	140	
gac acc aag atg cct aca aca gaa aga gaa	aca gaa ctc gct gtg tct	480	
Asp Thr Lys Met Pro Thr Glu Arg Glu Thr	Glu Leu Ala Val Ser		
145	150	155	160
gag gag cag agg gtg gag ctc agc atc tct ctg	ata aac cag agg ttc	528	
Glu Glu Gln Arg Val Glu Leu Ser Ile Ser	Leu Ile Asn Gln Arg Phe		
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Glu Ala Val Trp Glu Ala Tyr Arg Ile Phe Leu Asp Arg Ile Pro Asp		
35	40	45

Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe		
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Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu			
65	70	75	80

Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys		
85	90	95

Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile		
100	105	110

Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val		
115	120	125

Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile Leu Asp Asn Ala Leu Asn		
130	135	140

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agccaga atg tat ttg gaa act aga aga gct att ttt gtt ttt tgg att 169
Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile
1 5 10
ttt ctc caa gtt caa gga act aaa gat atc tcc att aac ata tac cat 217
Phe Leu Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His
15 20 25 30
tct gaa act aaa gac ata gac aat ccc cca aga aat gaa aca act gaa 265
Ser Glu Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu
35 40 45
agt act gaa aaa atg tac aaa atg tca act atg aga cga ata ttc gat 313
Ser Thr Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp
50 55 60
ttg gca aag cat cga aca aaa aga tcc gca ttt ttc cca acg ggg gtt 361
Leu Ala Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val
65 70 75
aaa gtc tgt cca cag gaa tcc atg aaa cag att tta gac agt ctt caa 409
Lys Val Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln
80 85 90
gct tat tat aga ttg aga gtg tgt cag gaa gca gta tgg gaa gca tat 457
Ala Tyr Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr
95 100 105 110
cgg atc ttt ctg gat cgc atc cct gac aca ggg gaa tat cag gac tgg 505
Arg Ile Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp
115 120 125
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Val Ser Ile Cys Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys
130 135 140
aac ttc agc aat tcc cag gag cac ctg gat ctt ctc cag cag aga ata 601
Asn Phe Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile
145 150 155

aaa cag aga agt ttc cct gac aga	aaa gat gaa ata tct gca gag aag	649	
Lys Gln Arg Ser Phe Pro Asp Arg	Lys Asp Glu Ile Ser Ala Glu Lys		
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aca ttg gga gag cct ggt gaa acc	att gtc att tca aca gat gtt gcc	697	
Thr Leu Gly Glu Pro Gly Glu Thr	Ile Val Ile Ser Thr Asp Val Ala		
175	180	185	190
aac gtc tca ctt ggg cct ttc cct	act cct gat gac acc ctc ctc	745	
Asn Val Ser Leu Gly Pro Phe Pro	Leu Thr Pro Asp Asp Thr Leu Leu		
195	200	205	
aat gaa att ctc gat aat aca ctc	aac gac acc aag atg cct aca aca	793	
Asn Glu Ile Leu Asp Asn Thr Leu	Asn Asp Thr Lys Met Pro Thr Thr		
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gaa aga gaa aca gaa ttc gct	gtg ttg gag gag cag agg gtg gag ctc	841	
Glu Arg Glu Thr Glu Phe Ala Val	Leu Glu Glu Gln Arg Val Glu Leu		
225	230	235	
agc gtc tct ctg gta aac cag	aag ttc aag gca gag ctc gct gac tcc	889	
Ser Val Ser Leu Val Asn Gln	Lys Phe Lys Ala Glu Leu Ala Asp Ser		
240	245	250	
cag tcc cca tat tac cag gag	cta gca gga aag tcc caa ctt cag atg	937	
Gln Ser Pro Tyr Tyr Gln Glu Leu	Ala Gly Lys Ser Gln Leu Gln Met		
255	260	265	270
caa aag ata ttt aag aaa ctt cca	gga ttc aaa aaa atc cat gtg tta	985	
Gln Lys Ile Phe Lys Lys Leu Pro	Gly Phe Lys Lys Ile His Val Leu		
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gga ttt aga cca aag aaa gaa	aaa gat ggc tca agc tcc aca gag atg	1033	
Gly Phe Arg Pro Lys Lys Glu Lys	Asp Gly Ser Ser Ser Thr Glu Met		
290	295	300	
caa ctt acg gcc atc ttt aag	aga cac agt gca gaa gca aaa agc cct	1081	
Gln Leu Thr Ala Ile Phe Lys Arg	His Ser Ala Glu Ala Lys Ser Pro		
305	310	315	
gca agt gac ctc ctg tct ttt	gat tcc aac aaa att gaa agt gag gaa	1129	
Ala Ser Asp Leu Leu Ser Phe Asp	Ser Asn Lys Ile Glu Ser Glu Glu		
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gtc tat cat gga acc atg gag	gag gac aag caa cca gaa atc tat ctc	1177	
Val Tyr His Gly Thr Met Glu Glu	Asp Lys Gln Pro Glu Ile Tyr Leu		
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aca gct aca gac ctc aaa agg	ctg atc agc aaa gca cta gag gaa gaa	1225	
Thr Ala Thr Asp Leu Lys Arg Leu	Ile Ser Lys Ala Leu Glu Glu Glu		
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caa tct ttg gat gtg ggg aca	att cag ttc act gat gaa att gct gga	1273	
Gln Ser Leu Asp Val Gly Thr Ile	Gln Phe Thr Asp Glu Ile Ala Gly		
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tca ctg cca gcc ttt ggt cct gac acc caa tca/gag	ctg ccc aca tct	1321
Ser Leu Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser		
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Phe Ala Val Ile Thr Glu Asp Ala Thr Leu/Ser Pro Glu Leu Pro Pro		
400	405	410
gtt gaa ccc cag ctt gag aca gtg gac gga gca gag cat ggt cta cct		1417
Val Glu Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro		
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430		
gac act tct tgg tct cca cct gct atg gcc tct acc tcc ctg tca gaa		1465
Asp Thr Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu		
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gct cca cct ttc ttt atg gca tca agc atc ttc tct ctg act gat caa		1513
Ala Pro Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln		
450	455	460
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Gly Thr Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly		
465	470	475
ctc acc atc ccc acc agt gat tat tct gca atc agc caa ctg gct ctg		1609
Leu Thr Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu		
480	485	490
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Gly Ile Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala		
495	500	505
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Gly Gly Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp		
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Thr Pro Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val		
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cca gat cat ttc ttg gag gat acc act cct gtc tca gct tta cag tat		1801
Pro Asp His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr		
545	550	555
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Ile Thr Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val		
565	570	
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Val Phe Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu		
575	580	590
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Phe Asn Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr		
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cag ctg ctg gtt cca tat cta cga tcc aat ctt aca gga	ttt aag caa	1993	
Gln Leu Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly	Phe Lys Gln		
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ctt gaa ata ctt aac ttc aga aac ggg agt gtg att	gtg aat agc aaa	2041	
Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Val Ile	Val Asn Ser Lys		
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atg aag ttt gct aag tct gtg ccg tat aac ctc acc aag	gct gtg cac	2089	
Met Lys Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys	Ala Val His		
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ggg gtc ttg gag gat ttt cgt tct gct gca	gcc caa caa ctc cat ctg	2137	
Gly Val Leu Glu Asp Phe Arg Ser Ala Ala	Gln Gln Leu His Leu		
655	660	665	670
gaa ata gac agc tac tct ctc aac att	gaa cca gct gat caa gca gat	2185	
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ccc tgc aag ttc ctg gcc tgc ggc gaa	ttt gcc caa tgt gta aag aac	2233	
Pro Cys Lys Phe Leu Ala Cys Gly	Glu Phe Ala Gln Cys Val Lys Asn		
690	695	700	
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Glu Arg Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro	Gly Tyr Asp Ser		
705	710	715	
cag ggg agc ctg gac ggt ctg gaa cca ggc ctc tgt	ggc ctg gca caa	2329	
Gln Gly Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly	Leu Ala Gln		
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agg aat gcg agg tcc tcc agg gaa agg gag ctc cat	gcg gtt cca gat	2377	
Arg Asn Ala Arg Ser Ser Arg Glu Arg Glu Leu His	Ala Val Pro Asp		
735	740	745	750
cac tct gaa aat caa gca tac aaa act agt gtt aaa	agt tcc aaa atc	2425	
His Ser Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys	Ser Ser Lys Ile		
755	760	765	
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Asn Lys Ile Thr Arg			
770			
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 35 40 45
 Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp Leu Ala
 50 55 60
 Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val Lys Val
 65 70 75 80
 Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln Ala Tyr
 85 90 95
 Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr Arg Ile
 100 105 110
 Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp Val Ser
 115 120 125
 Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe
 130 135 140
 Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln
 145 150 155 160
 Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys Thr Leu
 165 170 175
 Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala Asn Val
 180 185 190

Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu Asn Glu
 195 200 205

Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr Glu Arg
 210 215 220

Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu Ser Val
 225 230 235 240

Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser Gln Ser
 245 250 255

Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met Gln Lys
 260 265 270

Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu Gly Phe
 275 280 285

Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met Gln Leu
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Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro Ala Ser
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Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu Val Tyr
 325 330 335

His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu Thr Ala
 340 345 350

Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu Gln Ser
 355 360 365

Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly Ser Leu
 370 375 380

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 385 390 395 400

Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro Val Glu
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Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro Asp Thr
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Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu Ala Pro
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Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln Gly Thr
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Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly Leu Thr
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 515 520 525

Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val Pro Asp
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His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr Ile Thr
 545 550 555 560

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 565 570 575

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 610 615 620

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 625 630 635 640

Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His Gly Val
 645 650 655

Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu Glu Ile
 660 665 670

Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp Pro Cys
 675 680 685

Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn Glu Arg
 690 695 700

Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser Gln Gly
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Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln Arg Asn
 725 730 735

Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp His Ser
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 <212> DNA

<213> Homo sapiens

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<221> CDS

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tggaagttc aaggatttgg acactcaatt aaggatctg tccttcctc attccttgg 180

ttttggcca a atg att atg ttt ctt ttt ggg aag att tct ctg ggt 230
Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly

1 5 10

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Ile Leu Ile Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala
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Gln Thr Tyr Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val
30 35 40 45tct ttt ctc ctg cct gaa gaa tca aca gac ctt tct cta gct acc aaa 374
Ser Phe Leu Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys
50 55 60aag aaa cag cct ctg gac cgc aga gaa act gaa aga cag tgg tta atc 422
Lys Lys Gln Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile
65 70 75aga agg cgg aga tct att ctg ttt cct aat gga gtg aaa atc tgc cca 470
Arg Arg Arg Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro
80 85 90gat gaa agt gtt gca gag gct gtg gca aat cat gtg aag tat ttt aaa 518
Asp Glu Ser Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys
95 100 105gtc cga gtg tgt cag gaa gct gtc tgg gaa gcc ttc agg act ttt tgg 566
Val Arg Val Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp
110 115 120 125gat cga ctt cct ggg cgt gag gaa tat cat tac tgg atg aat ttg tgt 614
Asp Arg Leu Pro Gly Arg Glu Tyr His Tyr Trp Met Asn Leu Cys
130 135 140gag gat gga gtc aca agt ata ttt gaa atg ggc aca aat ttt agt gaa 662
Glu Asp Gly Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu
145 150 155

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Ser	Val	Glu	His	Arg	Ser	Leu	Ile	Met	Lys	Lys	Leu	Thr	Tyr	Ala	Lys	
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gaa	act	gta	agc	agc	tct	gaa	ctg	tct	tct	cca	gtt	cct	gtt	ggt	gat	758
Glu	Thr	Val	Ser	Ser	Ser	Glu	Leu	Ser	Ser	Pro	Val	Pro	Val	Gly	Asp	
175						180				185						
act	tca	aca	ttg	gga	gac	act	act	ctc	agt	gtt	cca	cat	cca	gag	gtg	806
Thr	Ser	Thr	Leu	Gly	Asp	Thr	Thr	Leu	Ser	Val	Pro	His	Pro	Glu	Val	
190						195				200				205		
gac	gcc	tat	gaa	ggt	gcc	tca	gag	agc	agc	ttg	gaa	agg	cca	gag	gag	854
Asp	Ala	Tyr	Glu	Gly	Ala	Ser	Glu	Ser	Ser	Leu	Glu	Arg	Pro	Glu	Glu	
						210			215				220			
agt	att	agc	aat	gaa	att	gag	aat	gtg	ata	gaa	gaa	gcc	aca	aaa	cca	902
Ser	Ile	Ser	Asn	Glu	Ile	Glu	Asn	Val	Ile	Glu	Glu	Ala	Thr	Lys	Pro	
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gca	ggg	gaa	cag	att	gca	gaa	tcc	agt	atc	cac	ctt	ttg	ggg	aag	cag	950
Ala	Gly	Glu	Gln	Ile	Ala	Glu	Phe	Ser	Ile	His	Leu	Leu	Gly	Lys	Gln	
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tac	agg	gaa	gaa	cta	cag	gat	tcc	tcc	agc	ttt	cac	cac	cag	cac	ctt	998
Tyr	Arg	Glu	Glu	Leu	Gln	Asp	Ser	Ser	Ser	Phe	His	His	Gln	His	Leu	
						255			260				265			
gaa	gaa	gaa	ttt	att	tca	gag	gtt	gaa	aat	gca	ttt	act	ggg	tta	cca	1046
Glu	Glu	Glu	Phe	Ile	Ser	Glu	Val	Glu	Asn	Ala	Phe	Thr	Gly	Leu	Pro	
						270			275				280		285	
ggc	tac	aag	gaa	att	cgt	gta	ctt	gaa	ttt	agg	tcc	ccc	aag	gaa	aat	1094
Gly	Tyr	Lys	Glu	Ile	Arg	Val	Leu	Glu	Phe	Arg	Ser	Pro	Lys	Glu	Asn	
						290			295				300			
gac	agt	ggc	gta	gat	gtt	tac	tat	gca	gtt	acc	tcc	aat	ggt	gag	gcc	1142
Asp	Ser	Gly	Val	Asp	Val	Tyr	Tyr	Ala	Val	Thr	Phe	Asn	Gly	Glu	Ala	
						305			310				315			
atc	agc	aat	acc	acc	tgg	gac	ctc	att	agc	ctt	cac	tcc	aac	aag	gtg	1190
Ile	Ser	Asn	Thr	Thr	Trp	Asp	Leu	Ile	Ser	Leu	His	Ser	Asn	Lys	Val	
						320			325				330			
gaa	aac	cat	ggc	ctt	gtg	gaa	ctg	gat	gat	aaa	ccc	act	gtt	gtt	tat	1238
Glu	Asn	His	Gly	Leu	Val	Glu	Leu	Asp	Asp	Lys	Pro	Thr	Val	Val	Tyr	
						335			340				345			
aca	atc	agt	aac	tcc	aga	gat	tat	att	gct	gag	aca	ttg	cag	cag	aat	1286
Thr	Ile	Ser	Asn	Phe	Arg	Asp	Tyr	Ile	Ala	Glu	Thr	Leu	Gln	Gln	Asn	
						350			355				360		365	
ttt	ttg	ctg	ggg	aac	tct	tcc	ttg	aat	cca	gat	cct	gat	tcc	ctg	cag	1334
Phe	Leu	Leu	Gly	Asn	Ser	Ser	Leu	Asn	Pro	Asp	Pro	Asp	Ser	Leu	Gln	
						370			375				380			

ctt atc aat gtg aga gga gtt ttg cgt cac	caa act gaa gat cta gtt	1382	
Leu Ile Asn Val Arg Gly Val Leu Arg His	Gln Thr Glu Asp Leu Val		
385	390	395	
tgg aac acc caa agt tca agt ctt cag gca acg ccg tca tct att ctg		1430	
Trp Asn Thr Gln Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu			
400	405	410	
gat aat acc ttt caa gct gca tgg ccc tca gca gat gaa tcc atc acc		1478	
Asp Asn Thr Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr			
415	420	425	
agc agt att cca cca ctt gat ttc agc tct ggt cct ccc tca gcc act		1526	
Ser Ser Ile Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr			
430	435	440	445
ggc agg gaa ctc tgg tca gaa agt cct ttg ggt gat tta gtg tct aca		1574	
Gly Arg Glu Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr			
450	455	460	
cac aaa tta gcc ttt ccc tcg aag atg ggc ctc agc tct tcc cca gag		1622	
His Lys Leu Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu			
465	470	475	
gtt tta gag gtt agc agc ttg act ctt cat tct gtc acc ccg gca gtg		1670	
Val Leu Glu Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val			
480	485	490	
ctt cag act ggc ttg cct gtg gct tct gag gaa agg act tct gga tct		1718	
Leu Gln Thr Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser			
495	500	505	
cac ttg gta gaa gat gga tta gcc aat gtt gaa gag tca gaa gat ttt		1766	
His Leu Val Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe			
510	515	520	525
ctt tct att gat tca ttg cct tca agt tca ttc act caa cct gtg cca		1814	
Leu Ser Ile Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro			
530	535	540	
aaa gaa aca ata cca tcc atg gaa gac tct gat gtg tcc tta aca tct		1862	
Lys Glu Thr Ile Pro Ser Met Glu Asp Ser Asp Val Ser Leu Thr Ser			
545	550	555	
tca cca tat ctg acc tct tct ata cct ttt ggc ttg gac tcc ttg acc		1910	
Ser Pro Tyr Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr			
560	565	570	
tcc aaa gtc aaa gac caa tta aaa gtg agc cct ttc ctg cca gat gca		1958	
Ser Lys Val Lys Asp Gln Leu Lys Val Ser Pro Phe Leu Pro Asp Ala			
575	580	585	
tcc atg gaa aaa gag tta ata ttt gac ggt ggt tta ggt tca ggg tct		2006	
Ser Met Glu Lys Glu Leu Ile Phe Asp Gly Gly Leu Gly Ser Gly Ser			
590	595	600	605

13

ggg caa aag gta gat ctg att act tgg cca tgg agt gag act tca tca	2054
Gly Gln Lys Val Asp Leu Ile Thr Trp Pro Trp Ser Glu Thr Ser Ser	
610 615 620	
gag aag agc gcc gaa cca ctg tcc aag ccg tgg ctt gaa gat gat gat	2102
Glu Lys Ser Ala Glu Pro Leu Ser Lys Pro Trp Leu Glu Asp Asp Asp	
625 630 635	
tca ctt ttg cca gct gag att gaa gac aag aaa cta gtt tta gtt gac	2150
Ser Leu Leu Pro Ala Glu Ile Glu Asp Lys Lys Leu Val Leu Val Asp	
640 645 650	
aaa atg gat tcc aca gac caa att agt aag cac tca aaa tat gaa cat	2198
Lys Met Asp Ser Thr Asp Gln Ile Ser Lys His Ser Lys Tyr Glu His	
655 660 665	
gat gac aga tcc aca cac ttt cca gag gaa gag cct ctt agt ggg cct	2246
Asp Asp Arg Ser Thr His Phe Pro Glu Glu Pro Leu Ser Gly Pro	
670 675 680 685	
gct gtg ccc atc ttc gca gat act gca gct gaa tct gcg tct cta acc	2294
Ala Val Pro Ile Phe Ala Asp Thr Ala Ala Glu Ser Ala Ser Leu Thr	
690 695 700	
ctc ccc aag cac ata tca gaa gta cct ggt gtt gat gat tgc tca gtt	2342
Leu Pro Lys His Ile Ser Glu Val Pro Gly Val Asp Asp Cys Ser Val	
705 710 715	
acc aaa gca cct ctt ata ctg aca tct gta gca atc tct gcc tct act	2390
Thr Lys Ala Pro Leu Ile Leu Thr Ser Val Ala Ile Ser Ala Ser Thr	
720 725 730	
gat aaa tca gat cag gca gat gcc atc cta agg gag gat atg gaa caa	2438
Asp Lys Ser Asp Gln Ala Asp Ala Ile Leu Arg Glu Asp Met Glu Gln	
735 740 745	
att act gag tca tcc aac tat gaa tgg ttt gac agt gag gtt tca atg	2486
Ile Thr Glu Ser Ser Asn Tyr Glu Trp Phe Asp Ser Glu Val Ser Met	
750 755 760 765	
gta aag cca gat atg caa act ttg tgg act ata ttg cca gaa tca gag	2534
Val Lys Pro Asp Met Gln Thr Leu Trp Thr Ile Leu Pro Glu Ser Glu	
770 775 780	
aga gtt tgg aca aga act tct tcc cta gag aaa ttg tcc aga gac ata	2582
Arg Val Trp Thr Arg Thr Ser Ser Leu Glu Lys Leu Ser Arg Asp Ile	
785 790 795	
ttg gca agt aca cca cag agt gct gac agg ctc tgg tta tct gtg aca	2630
Leu Ala Ser Thr Pro Gln Ser Ala Asp Arg Leu Trp Leu Ser Val Thr	
800 805 810	
cag tct acc aaa ttg cct cca acc aca atc tcc acc ctg cta gag gat	2678
Gln Ser Thr Lys Leu Pro Pro Thr Thr Ile Ser Thr Leu Leu Glu Asp	
815 820 825	

gaa gta att atg ggt gta cag gat att tcg tta gaa ctg gac cg	gata	2726	
Glu Val Ile Met Gly Val Gln Asp Ile Ser Leu Glu Leu Asp Arg Ile			
830	835	840	845
ggc aca gat tac tat cag cct gag caa gtc caa gag caa aat ggc aag		2774	
Gly Thr Asp Tyr Tyr Gln Pro Glu Gln Val Gln Glu Gln Asn Gly Lys			
850	855	860	
gtt ggt agt tat gtg gaa atg tca aca agt gtt cac tcc aca gag atg		2822	
Val Gly Ser Tyr Val Glu Met Ser Thr Ser Val His Ser Thr Glu Met			
865	870	875	
gtt agt gtg gct tgg ccc aca gaa gga gga gat gac ttg agt tat acc		2870	
Val Ser Val Ala Trp Pro Thr Glu Gly Gly Asp Asp Leu Ser Tyr Thr			
880	885	890	
cag act tca gga gct ttg gtg gtt ttc ttc agc ctc cga gtg act aac		2918	
Gln Thr Ser Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val Thr Asn			
895	900	905	
atg atg ttt tca gaa gat ctg ttt aat aaa aac tcc ttg gag tat aaa		2966	
Met Met Phe Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu Tyr Lys			
910	915	920	925
gcc ctg gag caa aga ttc tta gaa ttg ctg gtt ccc tat ctc cag tca		3014	
Ala Leu Glu Gln Arg Phe Leu Glu Leu Leu Val Pro Tyr Leu Gln Ser			
930	935	940	
aat ctc acg ggg ttc cag aac tta gaa atc ctc aac ttc aga aat ggc		3062	
Asn Leu Thr Gly Phe Gln Asn Leu Glu Ile Leu Asn Phe Arg Asn Gly			
945	950	955	
agc att gtg gtg aac agt cga atg aag ttt gcc aat tct gtc cct cct		3110	
Ser Ile Val Val Asn Ser Arg Met Lys Phe Ala Asn Ser Val Pro Pro			
960	965	970	
aac gtc aac aat gcg gtg tac atg att ctg gaa gac ttt tgt acc act		3158	
Asn Val Asn Asn Ala Val Tyr Met Ile Leu Glu Asp Phe Cys Thr Thr			
975	980	985	
gcc tac aat acc atg aac ttg gct att gat aaa tac tct ctt gat gtg		3206	
Ala Tyr Asn Thr Met Asn Leu Ala Ile Asp Lys Tyr Ser Leu Asp Val			
990	995	1000	1005
gaa tca ggt gat gaa gcc aac cct tgc aag ttt cag gcc tgt aat gaa		3254	
Glu Ser Gly Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys Asn Glu			
1010	1015	1020	
ttt tca gag tgt ctg gtc aac ccc tgg agt gga gaa gca aag tgc aga		3302	
Phe Ser Glu Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys Cys Arg			
1025	1030	1035	
tgc ttc cct gga tac ctg agt gtg gaa gaa cgg ccc tgt cag agt ctc		3350	
Cys Phe Pro Gly Tyr Leu Ser Val Glu Glu Arg Pro Cys Gln Ser Leu			
1040	1045	1050	

tgt gac cta cag cct gac ttc tgc ttg aat gat gga aag tgt gac att Cys Asp Leu Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys Asp Ile 1055 1060 1065	3398
atg cct ggg cac ggg gcc att tgt agg tgc cgg gtg ggt gag aac tgg Met Pro Gly His Gly Ala Ile Cys Arg Cys Arg Val Gly Glu Asn Trp 1070 1075 1080 1085	3446
tgg tac cga ggc aag cac tgt gag gaa ttt gtg tct gag ccc gtg atc Trp Tyr Arg Gly Lys His Cys Glu Glu Phe Val Ser Glu Pro Val Ile 1090 1095 1100	3494
ata ggc atc act att gcc tcc gtg gtt gga ctt ctt gtc atc ttt tct Ile Gly Ile Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser 1105 1110 1115	3542
gct atc atc tac ttc ttc atc agg act ctt caa gca cac cat gac agg Ala Ile Ile Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg 1120 1125 1130	3590
agt gaa aga gag agt ccc ttc agt ggc tcc agc agg cag cct gac agc Ser Glu Arg Glu Ser Pro Phe Ser Gly Ser Ser Arg Gln Pro Asp Ser 1135 1140 1145	3638
ctc tca tct att gag aat gct gtg aag tac aac ccc gtg tat gaa agt Leu Ser Ser Ile Glu Asn Ala Val Lys Tyr Asn Pro Val Tyr Glu Ser 1150 1155 1160 1165	3686
cac agg gct gga tgt gag aag tat gag gga ccc tat cct cag cat ccc His Arg Ala Gly Cys Glu Lys Tyr Glu Gly Pro Tyr Pro Gln His Pro 1170 1175 1180	3734
ttc tac agc tct gct agc gga gac gtg att ggt ggg ctg agc aga gaa Phe Tyr Ser Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu 1185 1190 1195	3782
gaa atc aga cag atg tat gag agc agt gag ctt tcc aga gag gaa att Glu Ile Arg Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile 1200 1205 1210	3830
caa gag aga atg aga gtt ttg gaa ctg tat gcc aat gat cct gag ttt Gln Glu Arg Met Arg Val Leu Glu Leu Tyr Ala Asn Asp Pro Glu Phe 1215 1220 1225	3878
gca gct ttt gtg aga gag caa caa gtg gaa gag gtt taacccaaaac Ala Ala Phe Val Arg Glu Gln Gln Val Glu Glu Val 1230 1235 1240	3924
tcctgttctg aaactgatta gaagcctgga gaagatggag attacttgtt acttatgtca 3984	
tataattaac ctggattta aacactgttg gaagaagagn tttctatgaa aaaattaaat 4044	
atagggcaca ctgtttttt ttcagcttaa gntttcagaa tgttagtnaga gatgtwmcat 4104	
ttttatcttataaagactg aatgctgtgt ttaaataatt gaaaactacg ttaaaaaaaaa 4164	
a	4165

<210> 6
<211> 1241
<212> PRT
<213> Homo sapiens

<400> 6
Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly Ile Leu Ile
1 5 10 15
Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr
20 25 30
Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu
35 40 45
Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln
50 55 60
Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile Arg Arg Arg
65 70 75 80
Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser
85 90 95
Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val
100 105 110
Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp Asp Arg Leu
115 120 125
Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys Glu Asp Gly
130 135 140
Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu Ser Val Glu
145 150 155 160
His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys Glu Thr Val
165 170 175
Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp Thr Ser Thr
180 185 190
Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val Asp Ala Tyr
195 200 205
Glu Gly Ala Ser Glu Ser Ser Leu Glu Arg Pro Glu Glu Ser Ile Ser
210 215 220
Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro Ala Gly Glu
225 230 235 240
Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln Tyr Arg Glu
245 250 255
Glu Leu Gln Asp Ser Ser Ser Phe His His Gln His Leu Glu Glu Glu
260 265 270

Phe Ile Ser Glu Val Glu Asn Ala Phe Thr Gly Leu Pro Gly Tyr Lys
 275 280 285

Glu Ile Arg Val Leu Glu Phe Arg Ser Pro Lys Glu Asn Asp Ser Gly
 290 295 300

Val Asp Val Tyr Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn
 305 310 315 320

Thr Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His
 325 330 335

Gly Leu Val Glu Leu Asp Asp Lys Pro Thr Val Val Tyr Thr Ile Ser
 340 345 350

Asn Phe Arg Asp Tyr Ile Ala Glu Thr Leu Gln Gln Asn Phe Leu Leu
 355 360 365

Gly Asn Ser Ser Leu Asn Pro Asp Pro Asp Ser Leu Gln Leu Ile Asn
 370 375 380

Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val Trp Asn Thr
 385 390 395 400

Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu Asp Asn Thr
 405 410 415

Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr Ser Ser Ile
 420 425 430

Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr Gly Arg Glu
 435 440 445

Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr His Lys Leu
 450 455 460

Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu Val Leu Glu
 465 470 475 480

Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val Leu Gln Thr
 485 490 495

Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser His Leu Val
 500 505 510

Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe Leu Ser Ile
 515 520 525

Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro Lys Glu Thr
 530 535 540

Ile Pro Ser Met Glu Asp Ser Asp Val Ser Leu Thr Ser Ser Pro Tyr
 545 550 555 560

Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr Ser Lys Val
 565 570 575

Lys	Asp	Gln	Leu	Lys	Val	Ser	Pro	Phe	Leu	Pro	Asp	Ala	Ser	Met	Glu
580								585						590	
Lys	Glu	Leu	Ile	Phe	Asp	Gly	Gly	Leu	Gly	Ser	Gly	Ser	Gly	Gln	Lys
595						600								605	
Val	Asp	Leu	Ile	Thr	Trp	Pro	Trp	Ser	Glu	Thr	Ser	Ser	Glu	Lys	Ser
610						615								620	
Ala	Glu	Pro	Leu	Ser	Lys	Pro	Trp	Leu	Glu	Asp	Asp	Asp	Ser	Leu	Leu
625						630				635				640	
Pro	Ala	Glu	Ile	Glu	Asp	Lys	Lys	Leu	Val	Leu	Val	Asp	Lys	Met	Asp
645								650						655	
Ser	Thr	Asp	Gln	Ile	Ser	Lys	His	Ser	Lys	Tyr	Glu	His	Asp	Asp	Arg
660								665						670	
Ser	Thr	His	Phe	Pro	Glu	Glu	Glu	Pro	Leu	Ser	Gly	Pro	Ala	Val	Pro
675						680							685		
Ile	Phe	Ala	Asp	Thr	Ala	Ala	Glu	Ser	Ala	Ser	Leu	Thr	Leu	Pro	Lys
690						695							700		
His	Ile	Ser	Glu	Val	Pro	Gly	Val	Asp	Asp	Cys	Ser	Val	Thr	Lys	Ala
705						710							720		
Pro	Leu	Ile	Leu	Thr	Ser	Val	Ala	Ile	Ser	Ala	Ser	Thr	Asp	Lys	Ser
725								730						735	
Asp	Gln	Ala	Asp	Ala	Ile	Leu	Arg	Glu	Asp	Met	Glu	Gln	Ile	Thr	Glu
740								745						750	
Ser	Ser	Asn	Tyr	Glu	Trp	Phe	Asp	Ser	Glu	Val	Ser	Met	Val	Lys	Pro
755						760							765		
Asp	Met	Gln	Thr	Leu	Trp	Thr	Ile	Leu	Pro	Glu	Ser	Glu	Arg	Val	Trp
770						775							780		
Thr	Arg	Thr	Ser	Ser	Leu	Glu	Lys	Leu	Ser	Arg	Asp	Ile	Leu	Ala	Ser
785						790							795		800
Thr	Pro	Gln	Ser	Ala	Asp	Arg	Leu	Trp	Leu	Ser	Val	Thr	Gln	Ser	Thr
805								810						815	
Lys	Leu	Pro	Pro	Thr	Thr	Ile	Ser	Thr	Leu	Leu	Glu	Asp	Glu	Val	Ile
820								825						830	
Met	Gly	Val	Gln	Asp	Ile	Ser	Leu	Glu	Leu	Asp	Arg	Ile	Gly	Thr	Asp
835								840						845	
Tyr	Tyr	Gln	Pro	Glu	Gln	Val	Gln	Glu	Gln	Asn	Gly	Lys	Val	Gly	Ser
850						855							860		
Tyr	Val	Glu	Met	Ser	Thr	Ser	Val	His	Ser	Thr	Glu	Met	Val	Ser	Val
865						870							875		880

Ala Trp Pro Thr Glu Gly Gly Asp Asp Leu Ser Tyr Thr Gln Thr Ser
 885 890 895

Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val Thr Asn Met Met Phe
 900 905 910

Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu Tyr Lys Ala Leu Glu
 915 920 925

Gln Arg Phe Leu Glu Leu Leu Val Pro Tyr Leu Gln Ser Asn Leu Thr
 930 935 940

Gly Phe Gln Asn Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Ile Val
 945 950 955 960

Val Asn Ser Arg Met Lys Phe Ala Asn Ser Val Pro Pro Asn Val Asn
 965 970 975

Asn Ala Val Tyr Met Ile Leu Glu Asp Phe Cys Thr Thr Ala Tyr Asn
 980 985 990

Thr Met Asn Leu Ala Ile Asp Lys Tyr Ser Leu Asp Val Glu Ser Gly
 995 1000 1005

Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys Asn Glu Phe Ser Glu
 1010 1015 1020

Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys Cys Arg Cys Phe Pro
 1025 1030 1035 1040

Gly Tyr Leu Ser Val Glu Glu Arg Pro Cys Gln Ser Leu Cys Asp Leu
 1045 1050 1055

Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys Asp Ile Met Pro Gly
 1060 1065 1070

His Gly Ala Ile Cys Arg Cys Arg Val Gly Glu Asn Trp Trp Tyr Arg
 1075 1080 1085

Gly Lys His Cys Glu Glu Phe Val Ser Glu Pro Val Ile Ile Gly Ile
 1090 1095 1100

Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser Ala Ile Ile
 105 1110 1115 1120

Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg Ser Glu Arg
 1125 1130 1135

Glu Ser Pro Phe Ser Gly Ser Ser Arg Gln Pro Asp Ser Leu Ser Ser
 1140 1145 1150

Ile Glu Asn Ala Val Lys Tyr Asn Pro Val Tyr Glu Ser His Arg Ala
 1155 1160 1165

Gly Cys Glu Lys Tyr Glu Gly Pro Tyr Pro Gln His Pro Phe Tyr Ser
 1170 1175 1180

Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu Glu Ile Arg
185 1190 1195 1200

Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile Gln Glu Arg
1205 1210 1215

Met Arg Val Leu Glu Leu Tyr Ala Asn Asp Pro Glu Phe Ala Ala Phe
1220 1225 1230

Val Arg Glu Gln Gln Val Glu Glu Val
1235 1240

<210> 7

<211> 20

<212> PRT

<213> rattus

<400> 7

Ser Ile Leu Phe Pro Asn Gly Val Arg Ile Cys Pro Ser Asp Thr Val
1 5 10 15

Ala Glu Ala Val
20

<210> 8

<211> 20

<212> PRT

<213> porcine

<220>

<221> UNSURE

<222> (1)..(20)

<223> applicants are unsure of residues designated as
"Xaa" at positions 1 & 11

<400> 8

Xaa Val Phe Phe Pro Thr Gly Val Lys Val Xaa Pro Gln Glu Ser Met
1 5 10 15

Lys Gln Ile Leu
20

<210> 9

<211> 10

<212> PRT

<213> porcine

<220>

<221> UNSURE

<222> (1)..(10)

<223> applicants are unsure of residues designated as
"Xaa" at position 1

<400> 9
Xaa Val Leu Phe Pro Asn Gly Val Lys/Ile
1 5 10

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> modified_base
<222> (25)
<223> i

<400> 10
tattaggaat tccatyttt tyccnaaygg

30

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> modified_base
<222> (1)..(26)
<223> "n" at positions 3, 6, 9 & 24 represent "inosine"

<400> 11
ttncncna gytcytgta rtangg

26

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
ggattttct ccaagttcaa gg

22

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
acgggggtta aagtctgtcc

20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
cgaacaaaaaa gatccgcatt

20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
ccttctgcct ctttgacatt g

21

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
atcaggactg ggtcagcatc

20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 17
tcaacagatg ttgccaaacgt

20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

23

<220>
<223> Description of Artificial Sequence: primer

<400> 18

gagcctggtg aaaccattgt

20

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

gtggagctca gcgtctctct

20

<210> 20

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20

tgtgttggag gagcagagg

19

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 21

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20

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

gaaacttcca ggattcaaaa aa

22

<210> 23

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<400> 23

aggaggacaa gcaaccagaa

20

<210> 24

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<400> 24

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22

<210> 25

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<400> 25

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20

<210> 26

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19

<210> 27

<211> 21

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21

<210> 28

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ctccctgtca gaagctccac 20

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<210> 33
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21

<210> 34
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<400> 34
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<210> 35
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<220>
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<400> 35
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<210> 36
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<220>
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<400> 36
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<210> 37
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<400> 37

gactgaggaa gcggagtg

<210> 38

<211> 18

<212> DNA

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<220>

<223> Description of Artificial Sequence: primer

<400> 38

acgaacggac tgaggaag

<210> 39

<211> 22

<212> DNA

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<220>

<223> Description of Artificial Sequence: primer

<400> 39

ttctgaatta ctgaccgtag aa

<210> 40

<211> 22

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<400> 40

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<210> 41

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<400> 41

ggtcataaaa atccagacat a

<210> 42

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27

<210> 43
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<220>
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<400> 43
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20

<210> 44
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<212> DNA
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<220>
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.<400> 44
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20

<210> 45
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 45
gcaggtctct ctaaacgcac g

21

<210> 46
<211> 15
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(15)
<223> applicants are unsure of residues designated as
"Xaa" at positions 1 & 11

<400> 46
Xaa Ala Leu Phe Pro Asn Gly Val Leu Ile Xaa Pro Xaa Glu Val
1 5 10 15

<210> 47

<211> 19
<212> PRT
<213> Callimico sp.

<220>
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<222> (1)..(19)
<223> applicants are unsure of residues designated as "Xaa" at positions 1, 11 & 16

<400> 47
Xaa Ile Leu Phe Pro Asn Gly Val Leu Ile Xaa Pro Asp Glu Val Xaa
1 5 10 15
Lys Glu Ile

<210> 48
<211> 20
<212> PRT
<213> Homo sapiens

<400> 48
Ser Ala Phe Phe Pro Thr Gly Val Lys Val Cys Pro Gln Glu Ser Met
1 5 10 15
Lys Gln Ile Leu
20

<210> 49
<211> 18
<212> PRT
<213> Callimico sp.

<220>
<221> UNSURE
<222> (1)..(18)
<223> applicants are unsure of residues designated as "Xaa" at positions 1 & 11

<400> 49
Xaa Ile Phe Phe Pro Thr Gly Val Lys Val Xaa Pro Gln Glu Ser Met
1 5 10 15
Lys Gln